

## STIC Biotechnology Systems Branch

### RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/507,416  
Source: PG 7/10  
Date Processed by STIC: 7/25/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/507,416

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length    The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering    The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4      Non-ASCII    The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5      Variable Length    Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"    A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7      Skipped Sequences  
    (OLD RULES)    Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
                           (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                           (i)       SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                           (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                           This sequence is intentionally skipped  
  
                           Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)    Sequence(s)      missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                           <210> sequence id number  
                           <400> sequence id number  
                           000
  
- 9      Use of n's or Xaa's  
    (NEW RULES)    Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                           Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                           In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10      Invalid <213>  
    Response    Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11      Use of <220>    Sequence(s)      missing the <220> "Feature" and associated numeric identifiers and responses.  
                           Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                           (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0  
    "bug"    Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa    "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/507,416

DATE: 07/25/2005

TIME: 08:51:42

Input Set : N:\Rasheed\PTO.SR.txt

Output Set: N:\CRF4\07252005\J507416.raw

3 <110> APPLICANT: GROSJEAN-COURNOYER, Marie-Claire  
 4 DENFERT, Christophe Didier  
 5 FIRON, Arnaud  
 6 VILLALBA, FranCois  
 7 LEBRUN, Marc-Henri  
 8 BEFFA, Roland  
 10 <120> TITLE OF INVENTION: Mutagenesis of Aspergillus fungi and identification  
 11 of genes essential for growth  
 13 <130> FILE REFERENCE: 346 723 - US  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/507,416  
 C--> 15 <141> CURRENT FILING DATE: 2004-09-13  
 15 <150> PRIOR APPLICATION NUMBER: PCT/IB 03/01 374  
 16 <151> PRIOR FILING DATE: 2003-03-13  
 18 <150> PRIOR APPLICATION NUMBER: US 60/363 543  
 19 <151> PRIOR FILING DATE: 2002-03-13  
 21 <150> PRIOR APPLICATION NUMBER: US 60/434 407  
 22 <151> PRIOR FILING DATE: 2002-12-19  
 24 <160> NUMBER OF SEQ ID NOS: 199  
 26 <170> SOFTWARE: PatentIn Ver. 3.2

*See item 4  
on Euro summary sheet*

*pp 1-4*

**Does Not Comply  
Corrected Diskette Needed**

## ERRORED SEQUENCES

10199 <210> SEQ ID NO: 199  
 10200 <211> LENGTH: 352  
 10201 <212> TYPE: PRT  
 10202 <213> ORGANISM: Aspergillus fumigatus  
 10204 <220> FEATURE:  
 10205 <223> OTHER INFORMATION: Homologue GmZnf1; Phylum CEA284.2;  
 10206 contig 4899 region 477626-479684  
 10207 Protein sequence  
 10209 <400> SEQUENCE: 199  
 10211 Met Ser Val Val Val Leu Val Ser Lys Pro Thr Ala His Phe Ser Glu  
 10212 1 5 10 15  
 10214 Leu Ala Ser His His Arg Val Arg Val Ile Ile Thr Leu Ala Lys Ala  
 10215 20 25 30  
 10217 Thr Met Ser His Pro Asp Leu Ser Thr Ile Leu Glu Val Tyr Pro Glu  
 10218 35 40 45  
 10220 Cys Glu Val Thr Cys Tyr Gly Tyr Ala Pro Ser Gln Arg Arg Arg Cys  
 10221 50 55 60  
 10223 Arg Met Arg Thr Arg Lys Asp Asn Arg Asp Arg Ala Ser Tyr Leu Leu  
 10224 65 70 75 80  
 10226 Glu Glu Gly Thr Arg Tyr Leu Gln Arg Gly Leu Pro Val Asp Gly Leu

*P2*

## RAW SEQUENCE LISTING

DATE: 07/25/2005

PATENT APPLICATION: US/10/507,416

TIME: 08:51:42

Input Set : N:\Rasheed\PTO.SR.txt

Output Set: N:\CRF4\07252005\J507416.raw

```

10227          85          90          95
10229 Leu Ile Glu Leu Ala Pro Leu Val Leu Cys Thr Arg Phe His Gln Tyr
10230          100          105          110
10232 Gln Ala Asp Asp Leu Val Arg Asp Trp Arg Ala Lys Leu Arg Glu Phe
10233          115          120          125
10235 Gln Gln Gln Thr Leu Leu Asn Ala Met Leu Lys Ser Leu Gln Glu Leu
10236          130          135          140
10238 Val Asp Ser Arg Ala Arg Ser Arg Ala Ala Arg Ser Ala Gly Arg Arg
10239 145          150          155          160
10241 Leu Pro Glu Arg Val Ser Ser Pro Thr Arg Leu Glu Arg Ser Ala Ala
10242          165          170          175
10244 Ile Val Thr Glu Glu Glu Pro Ala Ala Pro Glu Arg Glu Glu Glu Glu
10245          180          185          190
10247 Glu Glu Arg Gly Asp Arg Glu Asp Glu Pro Glu Pro Glu Pro Glu Pro
10248          195          200          205
10250 Glu Pro Glu Leu Thr Pro Ser Arg Ser Ser Thr Glu Thr Ser Ser Pro
10251          210          215          220
10253 Ala Val Glu Ala His Val Ala Glu Pro Thr Val Pro Gln Thr Glu Ser
10254 225          230          235          240
10256 Arg Arg Val Thr Arg Lys Pro Ile Glu Gly Asp Cys Thr Ile Cys Leu
10257          245          250          255
10259 Cys Pro Leu Arg Glu Gln Asp Ser Asp Glu Asn Gly Glu Gly Ser Glu
10260          260          265          270
10262 Asp Arg Asp Asp Glu Asn Glu Asp Asp Ala Ala Gly Thr Gly Ser Gly
10263          275          280          285
10265 Thr Ala Ser Asp Glu His Asp Ala Pro Glu Glu His Asp Asp Asp Asp
10266          290          295          300
10268 Leu Val Tyr Cys Lys Asn Gln Cys Gly Thr Asn Tyr His Lys Ala Cys
10269 305          310          315          320
10271 Ile Asp Val Trp His Ala Thr Gln Arg Thr Phe Glu Thr Pro Arg Gly
10272          325          330          335
10274 Asp Pro Ile Gly Leu Ser Cys Pro Tyr Cys Arg Ala Ala Trp Ser Ser
10275          340          345          350
E--> 10282

```

*delete**see p. 3*  
←

10/5 4/6

3

<210> 65  
<211> 35  
<212> DNA  
<213> Artificial sequence

change  
to

<220>  
<223> PCR primer PCRa1 1

↓  
<2217> <223> misc\_feature  
<2227> <223> (21)..(30)  
<223> n is a, c, g, or t

<400> 65  
ggccacgcgt cgactagtag nnnnnnnnnn gatat

35

This error appears in subsequent sequences

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

see p.4

VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/507,416

DATE: 07/25/2005

TIME: 08:51:44

Input Set : N:\Rasheed\PTO.SR.txt

Output Set: N:\CRF4\07252005\J507416.raw

FYI

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:65; N Pos. 21,22,23,24,25,26,27,28,29,30

Seq#:66; N Pos. 21,22,23,24,25,26,27,28,29,30

Seq#:67; N Pos. 21,22,23,24,25,26,27,28,29,30

Seq#:68; N Pos. 21,22,23,24,25,26,27,28,29,30

Seq#:171; N Pos. 683

Seq#:172; N Pos. 183

Seq#:173; N Pos. 183

**VERIFICATION SUMMARY**PATENT APPLICATION: **US/10/507,416**

DATE: 07/25/2005

TIME: 08:51:44

Input Set : **N:\Rasheed\PTO.SR.txt**Output Set: **N:\CRF4\07252005\J507416.raw**

L:15 M:270 C: Current Application Number differs, Replaced Current Application No  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:3463 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:65  
L:3464 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:65  
L:3464 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:65  
L:3464 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:65 after pos.:0  
L:3481 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:66  
L:3482 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:66  
L:3482 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:66  
L:3482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:66 after pos.:0  
L:3499 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:67  
L:3500 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:67  
L:3500 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:67  
L:3500 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:67 after pos.:0  
L:3517 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:68  
L:3518 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:68  
L:3518 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:68  
L:3518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:68 after pos.:0  
L:8642 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:171  
L:8642 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:171  
L:8642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:171 after pos.:660  
L:8678 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:172  
L:8678 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:172  
L:8678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:172 after pos.:180  
L:8705 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:173  
L:8705 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:173  
L:8705 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:173 after pos.:180  
L:10282 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:199